

Table 1. The EELL Motifs Occurring in the Crystal Structures and their Molecular Interactions

<i>Ec</i> ^a	Xtal ^b	Sequence (Xtal) ^c	Sequence Motif ^d	Structure Motif ^e	Interactions with			Loop ^g	Misc. ^h
					RNA	Proteins	Metal Ions ^f		
Conserved:									
16S 581	564	GUA/GAG	EL	EL	Yes	S15+S17	—	sI	SIF ²⁶
16S 685	668	GUA/GAU	EL	EL	Yes	S11	M ⁺	asI	SIF ²⁶ K ²¹
16S 765	748	GAA/CUA	EL	—	Yes	—	M ⁺	M	SIF ²⁶
16S 780	763	AAA/GUA	EL	EL	Yes	S11	M ⁺	sI	SIF ²⁶
16S 889	866	AGUA/GAA	E	E	Yes	—	M ⁺	asI	SIF ²⁶
16S 1304	1285	GGA/GAA	ELL	ELL	Yes	S13+THX	M ⁺	sI	
16S 1346	1327	AGUA/GAA	E	E	Yes	S7+S9	—	M	
23S 26	23	GGA/GAA	ELL	ELL	Yes	—	Mg ²⁺	sI	
23S 189	159	GAA/AGUA	E	E	Yes	L15e	Mg ²⁺	asI	
23S 241	212	AGUA/GAA	E	E	Yes	L15+L15e	Mg ²⁺	asI	
23S 298	304	GAA/GUA	EL	—	Yes	L4+L24	—	M	
23S 371	380	AGUA/GAA	E	E	Yes	L15e	—	M	
23S 457	463	AGUA/GAA	E	E	Yes	L4+L39e	Na ⁺	M	
23S 704	795	GAA/GGA	ELL	ELL	Yes	L19e+L37ae	Mg ²⁺	sI	
23S 818	911	GAA/AGUA	E	E [†]	Yes	L32e	Mg ²⁺ , Na ⁺	M	
23S 859	953	GUA/GAA	EL	E [†]	Yes	L21e	Mg ²⁺ , Na ⁺	sI	SIF (5S)
23S 1212	1316	GAA/GGA	ELL	ELL	Yes	L32e	—	asI	K ²¹
23S 1265	1369	AGUA/GAA	E	E	Yes	L22	Mg ²⁺	asI	
23S 1687	1765	GUA/GAA	EL	—	Yes	—	—	asI	SIF ²⁶
23S 1930	1971	GUA/GAA	EL	E [†]	Yes	—	Na ⁺	M	SIF ²⁶
23S 2467	2502	CAA/GAC	ELL	ELL	—	L10e	—	sI	
23S 2654	2691	AGUA/GAA	E	E	Yes	L6	—	asI	EFs ¹⁶
5S 76	77	AGUA/GAA	E	E	Yes	—	—	asI	SIF (23S)
Variable:									
16S 413	408	GAA/GUA	EL	—	Yes	S4	—	asI	
16S 447	441	GAC/GGUA	E	E	—	S16	—	asI	
16S 1238	1219	AA/AGU	E	E	Yes	S7	—	M	
23S 82	78	GGA/GAA	ELL	ELL	Yes	L24	—	asI	K ²¹
23S 286	292	GAC/AGUA	E	E	—	—	—	asI	
23S 544i.2	568	GAC/AGUA	E	E	—	L30	—	asI	
23S 635i	706	GCA/GAG	EL	EL	Yes	L18e	—	sI	
23S 844	937	CGA/GAC	ELL	ELL	Yes	—	—	asI	K ²¹
23S 1438	1543	GUC/CAA	EL	EL	Yes	—	—	sI	
23S 1484	1588	GGA/GAA	ELL	ELL	Yes	—	—	asI	K ²¹

^{a,b} The *Escherichia coli*-equivalent position numbers for the first nucleotides in the motifs and their corresponding position numbers in the rRNAs of the *T. thermophilus* 30S (PDB 1FJF¹⁹) and *H. marismortui* 50S (PDB 1JJ2²¹) crystal structures, respectively.

^c Nucleotide compositions in the current crystal structures being used, with the AGUA, GUA, and GGA sequences highlighted.

^{d,e} Sequence and structure motifs, respectively: E, AGUA/GAA motif; EL, GUA/GAA motif; ELL, GGA/GAA motif. The dagger marks (†) are used for the “transformed” motifs or the motifs which are formed differently from the predicted ones.

^f Each M⁺ represents a metal ion bound to the motifs but its identity was not determined in the crystal structure.

^g Loop type: sI, symmetric internal loop; asI, asymmetric internal loop; M, multistem loop.

^h Miscellaneous information: K, K-turn motif; SIF, present at the subunit interfaces; EFs, elongation factors.

Table 2. Phylogenetic Distribution and Frequencies of All EELL Motifs Identified in rRNAs[†]

<i>Ec</i> ^a	Motif ^b	A	B	E	C	M	<i>Ec</i> ^a	Motif ^b	A	B	E	C	M
Conserved:							23S 844	ELL	91.7	—	—	—	—
16S 581	EL	99.1	75.4	96.6	88.0	20.4	23S 1438	EL,ELL	X	X			
16S 685	EL,ELL	89.2	99.2	90.9	92.9	8.6	23S 1484*	ELL	100	—	—	—	—
16S 765	EL	99.5	97.3	93.0	94.1	31.9	23S 1710*	ELL	—	0.4	—	—	—
16S 780	EL	99.1	98.9	98.0	94.1	91.3	Variable (Others):						
16S 889	E	94.6	98.8	99.1	97.0	97.9	16S 68i	ELL			X		
16S 1304	ELL	94.7	99.4	95.7	95.4	79.0	16S 69i	E,ELL		X			
16S 1346	E	100	99.4	96.6	100	95.6	16S 70i	E,ELL		X	X		
23S 26	ELL	94.4	94.4	97.4	95.7	13.6	16S 73i	E,ELL		X			
23S 189	E	100	98.9	77.5	100	15.5	16S 74i	ELL		X			
23S 241	E	100	98.9	97.5	96.0	88.4	16S 76i	ELL		X			
23S 298	EL	100	95.3	46.2	95.0	5.1	16S 82i	ELL		X			
23S 371	E	100	99.6	97.3	98.0	11.3	16S 1441	ELL	—	—	85.1	—	—
23S 457	E	100	96.5	90.4	98.0	—	23S 294*	EL	29.7	40.9	—	12.6	—
23S 704	ELL	100	100	95.1	99.0	6.5	23S 544i.1	ELL	X				
23S 818	E	100	97.0	99.5	100	28.2	23S 641i	EL			X		
23S 859	EL	100	100	96.2	96.0	14.5	23S 1204i	ELL		X			
23S 1212	ELL	100	98.9	92.6	96.0	6.5	23S 1415i.1	ELL		X			
23S 1265	E	100	100	99.3	100	92.0	23S 1415i.2	E,ELL		X			
23S 1687	EL	78.1	74.1	62.6	91.1	7.6	23S 1418	ELL			X		
23S 1930	EL	100	97.9	99.4	99.0	96.8	23S 1475*	EL,ELL	—	39.4	2.8	—	—
23S 2467	ELL	100	99.6	99.3	100	66.2	23S 1526	ELL	—	57.0	—	9.0	—
23S 2654	E	100	100	100	100	98.8	23S 1529i	ELL		X			
5S 76 [‡]	E,EL	86.7	94.4	99.7	n/a	n/a	23S 1530i	E,ELL		X			
Variable (Xtal):							23S 1531i	ELL		X			
16S 413	EL	—	76.3	0.2	56.4	3.8	23S 1713	E,ELL		X			
16S 447	E	—	92.6	0.1	87.2	1.0	23S 1721	EL,ELL		9.5			
16S 661*	ELL	97.8	3.4	0.1	1.2	—	23S 1727i.1	EL		X			
16S 1238	E	98.6	98.6	0.4	97.7	3.2	23S 1727i.2	ELL			X		
16S 1260*	ELL	1.9	32.7	0.2	35.3	1.8	23S 1727i.3	ELL			X		
16S 1417*	ELL	—	0.2	—	—	0.5	23S 1727i.4	E			X		
23S 82	EL,ELL	100	93.4	0.8	95.4	1.3	23S 1857	ELL	—	93.1	—	—	4.2
23S 286	E,EL,ELL	7.7	3.9	2.0	—	—	23S 1865	ELL	—	—	—	3.9	—
23S 544i.2	E	91.9	—	—	0.1	—	23S 2133	ELL	53.7	93.5	—	57.8	0.7
23S 635i	EL	91.9	—	—	—	—	23S 2209i	E			X		

[†] Shown are the percentages for the frequencies of an EELL motif in each phylogenetic alignment of Archaea (A), Bacteria (B), Eukaryotes (E), Chloroplasts (C), and Mitochondria (M). The long dashes (—) represent the absence of the motifs in the current set of alignments. The motifs with the capital “X” marks are the motifs whose frequencies are not currently available.

^a The *Escherichia coli*-equivalent position numbers for the first nucleotides in the sequence motifs. The motifs present in the used crystal structures are shown in bold. The asterisk (*) marks are used for the motifs which exchange with either tandem GA motif or canonical basepairs in the rest of the sequences in the same or different phylogenetic groups.

^b Sequence motifs: E, AGUA/GAA motif; EL, GUA/GAA motif; ELL, GGA/GAA motif.

[‡] While the bacterial 5S rRNA has a GUA/GAA (EL) motif, the archaeal and eukaryotic 5S rRNAs have a AGUA/GAA (E) motif.